

[illegible]

Number of people with a college degree

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251 LTIGSNLSTRIAAYKSIQERVKKTWTVVDAKTLKKEDIQETVYCLNDD 300
|||||
251 LTIGSNLSTRIAAYKSIQERVKKTWTVVDAKTLKKEDIQETVYCLNDD 300
|||||
301 DETEVLKEDIQGFYGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCCKSSQ 350
|||||
301 DETEVLKEDIQGFYGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCCKSSQ 350
|||||
351 VQRRFFMGNOVLKVFAARDEAAAVALSLLIHALDDLDMVAIVRYAYDKR 400
|||||
351 VQRRFFMGNOVLKVFAARDEAAAVALSLLIHALDDLDMVAIVRYAYDKR 400
|||||
401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ 450
|||||
401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQ 450
|||||
451 INAVDALIDMSLAKKDEKDTLEDLFPTTKIPNPRFQRLFQ 492
|||||
451 INAVDALIDMSLAKKDEKDTLEDLFPTTKIPNPRFQRLFQ 492
|||||

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Fig. 1 (Cont.)

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1  MVRSGNKAADVLCMDVGTMTNSIPGIESPFQAKKVTIMFVQRQVFAEN 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MVRSGNKAADVLCMDVGTMTNSIPGIESPFQAKKVTIMFVQRQVFAEN 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 KDEIALVLFGTGTDNPLSGGDQYQNI TVHRHMLPDPFDLLEDIESKIQP 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 KDEIALVLFGTGTDNPLSGGDQYQNI TVHRHMLPDPFDLLEDIESKIQP 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 GSQQADFLDALIVSMDVIQHETIGKKFEKRHIETDLSSRFKSQLDII 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 GSQQADFLDALIVSMDVIQHETIGKKFEKRHIETDLSSRFKSQLDII 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 IHSKKCDISIQFFLPFSLGKEDSGDRGDGPFRLGGHGSPFPLKGITEQ 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 IHSKKCDISIQFFLPFSLGKEDSGDRGDGPFRLGGHGSPFPLKGITEQ 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLGVFKKIERHSIHWPGR 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLGVFKKIERHSIHWPGR 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Fig. 2.

251 LTIGSNLSIRIAAYKSIQERVKKTWVVDATAKLKKEDIQKETVYCLNDD 300  
 |||||  
 251 LTIGSNLSIRIAAYKSIQERVKKTWVVDATAKLKKEDIQKETVYCLNDD 300  
 301 DETE..... 304  
 ||||  
 301 DETEVLKEDIQGFYRGSDIVPFKVDDEEQMKYSEKCFSVLGECKSSQ 350  
 305 .....LNPPAEVTTKSQIPLSKIKITLPLIEAKKKDQVTA 339  
 |||||  
 501 PRELPPIQQHIWNMLNPPAEVTTKSQIPLSKIKITLPLIEAKKKDQVTA 550  
 340 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 389  
 |||||  
 551 QEIFQDNHEDGPTAKKLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 600  
 390 LVKQKKASFEASNLINHIETQFLDTNETPYFMKSIDCIRAFREEAIKFS 439  
 |||||  
 601 LVKQKKASFEASNLINHIETQFLDTNETPYFMKSIDCIRAFREEAIKFS 650

Fig. 2 (Cont.)

440 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGTILITKEEASGSSVTAAE 489  
 |||||  
 651 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGTILITKEEASGSSVTAAE 700  
 |||||  
 490 AKKFLAPKDKPSGDTAAVFEEGGDVDDLLDMI 521  
 |||||  
 701 AKKFLAPKDKPSGDTAAVFEEGGDVDDLLDMI 732

Fig. 2 (Cont.)

Fig. 3

252 GAGQFGEVWMGYNGHTKVAVKSLKQGSMPDAFLAEANIMKQLQHQLV 301  
 |||||  
 251 GAGQFGEVWMGYNGHTKVAVKSLKQGSMPDAFLAEANIMKQLQHQLV 300  
 |||||  
 302 RLYAVVTQEPYIITEYMEENGSLVDFLKTPSGIKLTINKLLDMAAQIAEG 351  
 |||||  
 301 RLYAVVTQEPYIITEYMEENGSLVDFLKTPSGIKLTINKLLDMAAQIAEG 350  
 |||||  
 352 MAFIERNYIHRDLRAANILVSDTLCKTADFGLARLIEDIHHQVR 397  
 ||||| : |  
 351 MAFIERNYIHRDLRAANILVSDTLCKTADFGLARLIEDNEYTAR 396

Fig. 3 (Cont.)

[illegible]

**Fig. 4 (Cont.)**



```

2  GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVY 51
   |||||||
1  GCGSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVY 50
   |||||||
52 EGSNPPASPIQDPQQGLKDKACGSLAVGFHLSPTYFLPGLAFLVPHV 101
   |||||||
51 EGSNPPASPIQ..... 61
102 TPGFIPIPARFSLTPLVFTDNLVIALHSYEPSHDGDLGFEKGEQLRILEQ 151
   |||||||
62 .....DNLVIALHSYEPSHDGDLGFEKGEQLRILEQ 92
152 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEPWFKNLSRKDAERQLLA 201
   |||||||
93 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEPWFKNLSRKDAERQLLA 142
202 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGGEVVKHYKIRNLNCGFYI 251
   |||||||
143 PGNTHGSFLIRESESTAGSFSLSVRDFDQNGGEVVKHYKIRNLNCGFYI 192
252 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTKPKPWWEDWEVPRE 301
   |||||||
193 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTKPKPWWEDWEVPRE 242

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Fig. 4

[illegible]

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62 AEAIPCTLAVSNPHTDAWKSHGLVEVASYCEESRGNNQWVPYISLQER 109
   | : | | |.||||| | | | | | | | | | | | | | | | | | | |
114 ARDLHC.LLVTNPHTDAWKSHGLVEVASYCEESRGNNQWVPYISLQER 160

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**Fig. 6**

```

1 MRAPPQVCEALLFALALQTVGYGIKWLALSKTPSALALNQTQHCQLEG 50
  |||||
1 MRARPOVCEALLFALALQTVGYGIKWLALSKTPSALALNQTQHCQLEG 50
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
101 LLDLERTRESAFVYALSAATISHAIAIACTSGDLPGCSCGPVGEPPGP 150
  |||||
101 LLDLERTRESAFVYALSAATISHAIAIACTSGDLPGCSCGPVGEPPGP 150
  |||||
151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKMLRLHNSVEGRQA 200
  |||||
151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKMLRLHNSVEGRQA 200
  |||||
201 LRASLEMKCKHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250
  |||||
201 LRASLEMKCKHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250
  |||||

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Fig. 7

```

251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300
|||||
251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300
|||||
301 KTSNGSDSCDLM.....CCVYTCRRCERTVER 327
|||||
301 KTSNGSDSCDLMCCGRGYNPYTDVVERCHCKYHWCCYVTCRRCERTVER 350
|||||
328 YVCK 331
|||||
351 YVCK 354

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**Fig. 7 (Cont.)**

1 MRARPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCKQLEG 50  
 |||||  
 1 MRARPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCKQLEG 50  
 |||||  
 51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100  
 |||||  
 51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100  
 |||||  
 101 LLDLERTRESAFVYA..... 116  
 |||||  
 101 LLDLERTRESAFVYALSAATISHAIARACTSGDLPGCSCGPVPEPPGP 150  
 |||||  
 117 .....AADLKTRYLSATKVVHR 133  
 |||||  
 201 LRASLEMKCKCHGVSGCSIRTCWKLQELQDVAADLKTRYLSATKVVHR 250  
 |||||  
 134 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN 183  
 |||||  
 251 PMGTRKHLVPKDLDIRPVKDWELVYLQSSPDFCMKNEKVGSHGTQDRQCN 300  
 |||||

Fig. 8

184 KTSNGSDSDLCCGGYNPYTDVVERCHKYHWCYVTCRRCERTVER 233  
 |||||  
 301 KTSNGSDSDLCCGGYNPYTDVVERCHKYHWCYVTCRRCERTVER 350

234 YVCK 237

\_\_\_\_\_

351 YVCK 354

**Fig. 8(Cont.)**

```

1 MSPFLRIGLSNFDGSCQCGEAVNPYCAVLKVEYVESENGOMYIQKP 50
  |||||
1 MSPFLRIGLSNFDGSCQCGEAVNPYCAVLKVEYVESENGOMYIQKP 50
  |||||

51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLSETTVELYSLAERCCKNN 100
  |||||
51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLSETTVELYSLAERCCKNN 100
  |||||

101 GKTEIWLELKPQGRMLMNARYFTLEMSDTKDMNEFETEGFFALHQRRGAIK 150
  |||||
101 GKTEIWLELKPQGRMLMNARYFTLEMSDTKDMNEFETEGFFALHQRRGAIK 150
  |||||

151 QAKVHVHKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200
  |||||
151 QAKVHVHKCHEFTATFFPQPTFCSVCHEFVWGLNKQGYQCRQCNAAIHKK 200
  |||||

201 CIDKVIACKTGSAINSRFTMFHKERFKIDMPHRFKVINYKSPTFCEHCGT 250
  |||||
201 CIDKVIACKTGSAINSRFTMFHKERFKIDMPHRFKVINYKSPTFCEHCGT 250
  |||||

251 LLWGLARQGLKCDACGMNVHRCQTKVANLCCGINOKLMAEALAMISTQQ 300
  |||||
251 LLWGLARQGLKCDACGMNVHRCQTKVANLCCGINOKLMAEALAMISTQQ 300
  |||||

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Fig. 9



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301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350
|||||
301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCPTPGKREPQGISWESPL 350
|||||
351 DEVDRMCHLPEPELNKERPSIQIKLIEDFILHKMLGKSGFGKVFLAEFK 400
|||||
351 DEVDRMCHLPEPELNKERPSIQIKLIEDFILHKMLGKSGFGKVFLAEFK 400
|||||
401 KTNQFFAIKALKKDVLMDDVECTMVEKRVLSLAWEHFELTHMFCFTQT 450
|||||
401 KTNQFFAIKALKKDVLMDDVECTMVEKRVLSLAWEHFELTHMFCFTQT 450
|||||
451 KENLFFVMEYLNCGDIMYHIQSCHKFDLSRATFYAAEIIIGLQFLHSGKI 500
|||||
451 KENLFFVMEYLNCGDIMYHIQSCHKFDLSRATFYAAEIIIGLQFLHSGKI 500
|||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
|||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550

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Fig. 9 (Cont.)

```

551 LLGQYNHSDWWSFGVLLYEMLLIGQSPFHGQDEEELFHSIRMDNPFYPR 600
    |||||
551 LLGQYNHSDWWSFGVLLYEMLLIGQSPFHGQDEEELFHSIRMDNPFYPR 600
    |||||

601 WLEKEAKDLLVKV 613
    |||||
601 WLEKEAKDLLVKL 613

```

Fig. 9(Cont.)

[illegible]

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1 MPITMRMRPWLEMQINSNOIPGLIWINKEEMIFOIPWKHAAKHGWDINK 50
  IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
1 MPITMRMRPWLEMQINSNOIPGLIWINKEEMILEIPWKHAAKHGWDINK 50
  .
51 DACLFERSWAIHTGRYKAGEKEPDPKTWKANFRCAMNSLPDIEEVKDQSRN 100
  IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
51 DACLFERSWAIHTGRYKAGEKEPDPKTWKANFRCAMNSLPDIEEVKDQSRN 100
  .
101 KGSSAVRVYRMLPPLTKNQRKERKSKSSRDAKSKAKRKSCGDSPTTSD 150
  IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
101 KGSSAVRVYRMLPPLTKNQRKERKSKSSRDAKSKAKRKSCGDSPTTSD 150
  .
151 GLSSSTLPDDHSSYTPVGYMQDLEVEQALTPALSPCAVSSSTLPDWHIPVE 200
  IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
151 GLSSSTLPDDHSSYTPVGYMQDLEVEQALTPALSPCAVSSSTLPDWHIPVE 200
  .
201 VVPDSTDLYNFQVSPMPSTSEATTDEDECKLPEDIMKILLEQSEWQPTN 250
  IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
201 VVPDSTDLYNFQVSPMPSTSEATTDEDECKLPEDIMKILLEQSEWQPTN 250
  .
      251 VDGKGYLLNEPGVQPTSVYGDFSCKEPEIDSPGG 285
        IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
      251 VDGKGYLLNEPGVQPTSVYGDFSCKEPEIDSPGG 285

```

**Fig. 10**



301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLS 350  
 |||||  
 301 GPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLS 350  
 |||||  
 351 HHSAWLTVLEALEERPAVMTSPLYLEIIITYCTGAFLISCMVGSVIVYKMK 400  
 |||||  
 351 HHSAWLTVLEALEERPAVMTSPLYLEIIITYCTGAFLISCMVGSVIVYKMK 400  
 |||||  
 401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLS 450  
 |||||  
 401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLS 450  
 |||||  
 451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCGQVVLAE AIGL 500  
 |||||  
 451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCGQVVLAE AIGL 500  
 |||||  
 501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEM MMKMI GKHKNIINLLGA 550  
 |||||  
 501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEM MMKMI GKHKNIINLLGA 550  
 |||||

Fig. 11 (Cont.)

551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSSKDL 600  
 |||||  
 551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSSKDL 600  
 601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDEVNPKIADFGIARDIHH 650  
 |||||  
 601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDEVNPKIADFGIARDIHH 650  
 651 IDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWSFGV 688  
 |||||  
 651 IDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWSFGV 688

Fig. 11(Cont.)

```

2 PKRGKKGVAEDGDDELRTPEAKKSKTAACKNDKEAAGEGPALYEDPPDQ 51
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 PKRGKKGVAEDGDDELRTPEAKKSKTAACKNDKEAAGEGPALYEDPPDQ 50
   .
52 KTSPSGKPATLKICSNNVDGLRAWIKKGLDWVKEAPDILCLQETKCSE 101
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 KTSPSGKPATLKICSNNVDGLRAWIKKGLDWVKEAPDILCLQETKCSE 100
   .
102 NKLPaelQLPGLSHQYWSAPSDKEGYSGVLRSQCPLKVSYGI..... 146
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 NKLPaelQLPGLSHQYWSAPSDKEGYSGVLRSQCPLKVSYGIGDEEH 150
   .
147 .....AYVPNAGRLVRLEYRQRWDEAFRKFLKLGLAS 178
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 DQeGRVIVAEFDfSVLVTAYVPNAGRLVRLEYRQRWDEAFRKFLKLGLAS 200
   .
179 RKPLVLCgDLNVAAHEEIDLrPKGNKNNAgtTPoERqCGFellQAVPlAD 228
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 RKPLVLCgDLNVAAHEEIDLrPKGNKNNAgtTPoERqCGFellQAVPlAD 250
```

Fig. 12

229 SFRHLYPNTPYAYTEFTWYMMNARSKNVGWRLDYFLLSHSLIPALCDISKIR 278  
 |||||  
 251 SFRHLYPNTPYAYTEFTWYMMNARSKNVGWRLDYFLLSHSLIPALCDISKIR 300  
 |||||  
 279 SKALGSDHCPITLYLAL 295  
 |||||  
 301 SKALGSDHCPITLYLAL 317

Fig. 12(Cont.)



```

2  PKRKKGVAEDGDELR TGKMK SALLPRNCGGVCHSLDVREPEAKSK 51
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  PKRKKGVAEDGDELR T.....EPEAKSK 26

52  TAAKKNDEAAGEPALYEDPPDQKTSPGKPA TLKICSNNVDGLRAWIK 101
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
27  TAAKKNDEAAGEPALYEDPPDQKTSPGKPA TLKICSNNVDGLRAWIK 76

102 KKGLDWVKEEAPDILCLQETKCSENKLPAELQELPGLSHQYWSAPSDKEG 151
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
77  KKGLDWVKEEAPDILCLQETKCSENKLPAELQELPGLSHQYWSAPSDKEG 126

152 YSGVLLSRQCLPKVSYGIGDEEHQDEGRVIVAEFDSFVLVTAYVFNAGR 201
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
127 YSGVLLSRQCLPKVSYGIGDEEHQDEGRVIVAEFDSFVLVTAYVFNAGR 176

202 GLVRLEYRQRWDEAFRFTLKG LASKRPLVLCGDLNVAHEEIDLNRPNKGNK 251
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
177 GLVRLEYRQRWDEAFRFTLKG LASKRPLVLCGDLNVAHEEIDLNRPNKGNK 226

```

Fig. 13

252 KNAGTPOERQGFCELLQAVPLADSFRLYPNTPIAYTFWTYMMNARSKN 301  
 |||||  
 227 KNAGTPOERQGFCELLQAVPLADSFRLYPNTPIAYTFWTYMMNARSKN 276  
 |||||  
 302 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL 342  
 |||||  
 277 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL 317

Fig. 13(Cont.)



251 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFFTE 300  
 |||||  
 251 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFFTE 300

301 DEV 303

||.

301 DEL 303

**Fig. 14 (Cont.)**

1 MFQAAERPPQEWAMEGFKUGUWAAAA  
1 MFQAAERPPQEWAMEGPRDGLKKERLLDDRHDSGLDSMKDEEYEQMVKELQ 50  
1 MFQAAERPPQEWAMEGPRDGLKKERLLDDRHDSGLDSMKDEEYEQMVKELQ 100  
51 EIRLEPQEVPRGSEPKQQLTEDGDSFLHLAIHEEKALTMVEIRQVKGD 100  
51 EIRLEPQEVPRGSEPKQQLTEDGDSFLHLAIHEEKALTMVEIRQVKGD 150  
101 LAFLNFQNNLQOTPLHLAVITNQPEIAEALLGAGCDPELDRFGNTPLHL 150  
101 LAFLNFQNNLQOTPLHLAVITNQPEIAEALLGAGCDPELDRFGNTPLHL 183  
151 ACEQGCLASGVLTQSCCTPHLSILKATNYG..... 200  
151 ACEQGCLASGVLTQSCCTPHLSILKATNYGHTCLHLASIHGILGIVE 200  
151 ACEQGCLASGVLTQSCCTPHLSILKATNYGHTCLHLASIHGILGIVE 222  
184 .....QEPNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250  
201 LVLVLGADVNAQEPNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250

Fig. 15

223 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFTTE 272  
 |||||  
 251 YSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFTTE 300  
 |||||  
 273 DELPYDDCVFGGQRLTL 289  
 |||||  
 301 DELPYDDCVFGGQRLTL 317

Fig. 15 (Cont.)



[illegible]

Fig. 16 (Cont.)



601 TYEDPNQAVREFAKEIDASCIEKVI GVGEFGEVCSGLKVP GKREICV 650  
 |||||  
 601 TYEDPNQAVREFAKEIDASCIEKVI GVGEFGEVCSGLKVP GKREICV 650  
 651 AIKTLKAGYTDKQRDFLSEASIMGQFDHPNIHLEGVVTKCKPVMITTE 700  
 |||||  
 651 AIKTLKAGYTDKQRDFLSEASIMGQFDHPNIHLEGVVTKCKPVMITTE 700  
 701 YMENGSLDAFLRKNDGRFTVIQLVGMLRGIGSGMKYLSDMSYVHRDLAAR 750  
 |||||  
 701 YMENGSLDAFLRKNDGRFTVIQLVGMLRGIGSGMKYLSDMSYVHRDLAAR 750  
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTGGKIPIRWTAPEAIAYRK 800  
 |||||  
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTGGKIPIRWTAPEAIAYRK 800  
 801 FTSASDVWSYGIWMVEVMSYGERPYWDMSNQD ..... 832  
 |||||  
 801 FTSASDVWSYGIWMVEVMSYGERPYWDMSNQDVTKAIEEGYRLPPMDCP 850  
 833 .....PNT 835  
 |||  
 851 IALHQLMLDCWQKERSDRPKFGQIVNMCLKLIRNPNSLKRGTGTESSRPNT 900

Fig. 16(Cont.)

[illegible]

Fig. 16 (Cont.)

[illegible]

Fig. 17

276 SLDDVQVPSEFEDDCQSCLNKPTMSFKDYIQERSDPVEQKPVIP 325  
 |||||  
 301 SLDDVQVPSEFEDDCQSCLNKPTMSFKDYIQERSDPVEQKPVIP 350  
 |||||  
 326 AAVLAGFTGSGPIQLWQFLLELLSDKSCQSFIWTGDGWEFKLADPDEVA 400  
 |||||  
 351 AAVLAGFTGSGPIQLWQFLLELLSDKSCQSFIWTGDGWEFKLADPDEVA 425  
 |||||  
 376 RRWGKRKNKPKMNYEKLRSGLRYYYDKNIIHKTSKRYVYRFVCDLQNL 450  
 |||||  
 401 RRWGKRKNKPKMNYEKLRSGLRYYYDKNIIHKTSKRYVYRFVCDLQNL 450  
 426 GETPEELHAILGVQPD TED 444  
 |||||  
 451 GETPEELHAILGVQPD TED 469

Fig. 17 (Cont.)



```

1  MALRRSMGRPGLPPLPPPPRLGILLAEAAAGLKMGA PVKLT VTSQGG 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MALRRSMGRPGLPPLPPPPRLGILLAEAAAGLKMGA PVKLT VTSQGG 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51  PVKLNCSEVGMEEPDIQWVKDGA VVQNLDQLYIPVSEQH WIGFSLKSVE 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51  PVKLNCSEVGMEEPDIQWVKDGA VVQNLDQLYIPVSEQH WIGFSLKSVE 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 RSDAGRYWCQVEDGGETEISQPVWLTVEGV PFFTV EPKDLAVPPNAPFQL 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 RSDAGRYWCQVEDGGETEISQPVWLTVEGV PFFTV EPKDLAVPPNAPFQL 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 SCEAVGPPEPVTIVWVRGTTKIGGPAPSPSVLNVTGVTQSTMFSCEAHNL 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 SCEAVGPPEPVTIVWVRGTTKIGGPAPSPSVLNVTGVTQSTMFSCEAHNL 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KGLASSRTATVHLQALPAAPFNITVTKLSSNASVAMWPGADGRALLQSC 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KGLASSRTATVHLQALPAAPFNITVTKLSSNASVAMWPGADGRALLQSC 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSLRVCANALGPSP 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSLRVCANALGPSP 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Fig. 19

```

301 YADWVPFQTKGLAPASAPQNLHAIRTDSCGILLEWEVPEAPLEGPLGY 350
|||||
301 YADWVPFQTKGLAPASAPQNLHAIRTDSCGILLEWEVPEAPLEGPLGY 350
|||||
351 KLSWQDNGTQDELTVEGTRANLTGWDPQKDLIVRVCVSNVAVGCGPWSQP 400
|||||
351 KLSWQDNGTQDELTVEGTRANLTGWDPQKDLIVRVCVSNVAVGCGPWSQP 400
|||||
401 LVVSSHDRAGQQGPPHSRTSWVPVLGVLTAIVTAAALAILLRKRKET 450
|||||
401 LVVSSHDRAGQQGPPHSRTSWVPVLGVLTAIVTAAALAILLRKRKET 450
|||||
451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLGIDELKEKL 500
|||||
451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLGIDELKEKL 500
|||||
501 EDVLIPEOQFTLGRMLGKGEFGSVREAQLKQEDGSFVKVAVKMLKADIIA 550
|||||
501 EDVLIPEOQFTLGRMLGKGEFGSVREAQLKQEDGSFVKVAVKMLKADIIA 550
|||||
551 SSDIEEFLREAAKKEFDHPHVAKLGVSLRSRAKGRLPIMPVILPFMKH 600
|||||
551 SSDIEEFLREAAKKEFDHPHVAKLGVSLRSRAKGRLPIMPVILPFMKH 600
|||||

```

Fig. 19 (Cont.)

601 GDLHAFLLASRIGENPFNLPLQTLIRFMVDIACGMEYLSRRNFIFHRDLAA 650  
 |||||  
 601 GDLHAFLLASRIGENPFNLPLQTLIRFMVDIACGMEYLSRRNFIFHRDLAA 650  
 |||||  
 651 RNCMLAEDMTVCVADFGLSRKIYSDCY 678  
 |||||  
 651 RNCMLAEDMTVCVADFGLSRKIYSGDY 678

Fig. 19 (Cont.)



1 MCRIAGALRTLLPLLAALLQASVEASGELALQASVTL 50  
 1 MCRIAGALRTLLPLLAALLQASVEASGEIALCKTFPEDVYSAVLSKDVH 50  
 1 MCRIAGALRTLLPLLAALLQASVEASGEIALCKTFPEDVYSAVLSKDVH 50  
 51 EQOPLLNVKFSNCNGKRKVQYESSEPADFKVDEGDMVYAVRSFPLSSEHA 100  
 51 EQOPLLNVKFSNCNGKRKVQYESSEPADFKVDEGDMVYAVRSFPLSSEHA 100  
 51 EQOPLLNVKFSNCNGKRKVQYESSEPADFKVDEGDMVYAVRSFPLSSEHA 100  
 101 KFLIYAQDKETQEKWQVAVKLSLKPILTEESVKESAEVEEIVFPQFSKH 150  
 101 KFLIYAQDKETQEKWQVAVKLSLKPILTEESVKESAEVEEIVFPQFSKH 150  
 101 KFLIYAQDKETQEKWQVAVKLSLKPILTEESVKESAEVEEIVFPQFSKH 150  
 151 SGHLQKQKRDWVIPPINLPENSRGPFPPQELVRIKSDRDKNLSLRYSTGP 200  
 151 SGHLQKQKRDWVIPPINLPENSRGPFPPQELVRIKSDRDKNLSLRYSTGP 200  
 201 GADQPPTGFIINPISGQSVTKPLDREQIARFHLRAHAVDINGNQVENP 250  
 201 GADQPPTGFIINPISGQSVTKPLDREQIARFHLRAHAVDINGNQVENP 250  
 251 IDIVINVIDMNDNRPEFLHQVWNGTVPEGSKPGTYMTVTAIDADDPNAL 300  
 251 IDIVINVIDMNDNRPEFLHQVWNGTVPEGSKPGTYMTVTAIDADDPNAL 300

Fig. 20

301	NGMLRYRIVSQAPSTPSPNMTTINNETGDIITVAAGLDREKVQOYTLIIQ	350
301	NGMLRYRIVSQAPSTPSPNMTTINNETGDIITVAAGLDREKVQOYTLIIQ	350
351	ATDMEGNPTYGLSNTATAVITVTDVNDNPPEFTAMTFYGEVPENRVDIIV	400
351	ATDMEGNPTYGLSNTATAVITVTDVNDNPPEFTAMTFYGEVPENRVDIIV	400
401	ANLTVTDKQDPHTPAWNAVYRISGGDPTGRFAIQITDPSNDGLVTVVVKPI	450
401	ANLTVTDKQDPHTPAWNAVYRISGGDPTGRFAIQITDPSNDGLVTVVVKPI	450
451	DFETNRMFVLTVAAENQVPLAKGIQHPQSTATVSVTVIDVNENPYFAPN	500
451	DFETNRMFVLTVAAENQVPLAKGIQHPQSTATVSVTVIDVNENPYFAPN	500
501	PKIIRQEEGLHAGTMLTTFTAQDPDRYMQONIRYTKLSDPANWLKIDPVN	550
501	PKIIRQEEGLHAGTMLTTFTAQDPDRYMQONIRYTKLSDPANWLKIDPVN	550
551	GQITTIIVLDRESPNVKNNIYNATFLASDNGICPPMSGTGTLQIYLLDIND	600
551	GQITTIIVLDRESPNVKNNIYNATFLASDNGICPPMSGTGTLQIYLLDIND	600

Fig. 20 (Cont.)

601 NAPQVLPQEAETCETPDNSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650  
 |||||  
 601 NAPQVLPQEAETCETPDNSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650  
 |||||  
 651 NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700  
 |||||  
 651 NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700  
 |||||  
 701 CQCDSNGDCTDVDRIVGAGLGTGAI IAILLCIIILLILVLMFVVMKRRD 750  
 |||||  
 701 CQCDSNGDCTDVDRIVGAGLGTGAI IAILLCIIILLILVLMFVVMKRRD 750  
 |||||  
 751 KERQAKQLLIDPEDDVRDNILKYDEEGGEEDQDYDLSQLQQPDTVEPDA 800  
 |||||  
 751 KERQAKQLLIDPEDDVRDNILKYDEEGGEEDQDYDLSQLQQPDTVEPDA 800  
 |||||  
 801 IKPVGIRRMDERPIHAEPQYFVRSAAAPHPGDIGDFINE 838  
 |||||  
 801 IKPVGIRRMDERPIHAEPQYFVRSAAAPHPGDIGDFINE 838  
 |||||

Fig. 20 (Cont.)



```

11 NVQILLEAASYLEQIEKENKCEHGYASSFSPMPRLQHSKPPRLSRA 60
   ||| ||| :||. |:| ||| ||| ||| ||| ||| ||| ||| |||
8 NVQRLLEAAEFLERRERE...CEHGYASSFSPMPRLQHSKPPRLSRA 54

61 QKHSSGSSNTSTANRSTHNELEKNRRAHLRLCLERLKVLIPLGPDCTRHT 110
   |||||. ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
55 QKHSSGTSNTSTANRSTHNELEKNRRAHLRLCLERLKVLIPLGPDCTRHT 104

111 TLGLLNKAKAHIKLEEAERKSQHOLENLEREQRFLLKWRLEQLQGPOEME 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
105 TLGLLNKAKAHIKLEEAERKSQHOLENLEREQRFLLKWRLEQLQGPOEME 154

161 RIRMDSIGSTISSDRSDSREEIEVDVESTEFSHGEVDNISTSIDIDD 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
155 RIRMDSIGSTISSDRSDSREEIEVDVESTEFSHGEVDNISTSIDIDD 204

211 HSSLPSIGSDEGYSSASVKLSFTS 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 HSSLPSIGSDEGYSSASVKLSFTS 228

```

Fig. 22

```

1 MESPASSQPASMPQSGKSKRKDLRISCMKPPAPNTPPRNLDSTFI 50
  |||||
1 MESPASSQPASMPQSGKSKRKDLRISCMKPPAPNTPPRNLDSTFI 50
  |||||

51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTMAVKRIRATVN 100
  |||||
51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTMAVKRIRATVN 100
  |||||

101 SEQKRLMLDLINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150
  |||||
101 SEQKRLMLDLINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150
  |||||

151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLSVIHRDVKPSNVLINK 200
  |||||
151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLSVIHRDVKPSNVLINK 200
  |||||

201 EGHVKMCDFGISGYLVDVSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250
  |||||
201 EGHVKMCDFGISGYLVDVSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250
  |||||

```

Fig. 23

251 VWSLGITMIEMAILRFPYESWGTFQQLKQVVVEEPPQLPADRFSPFVD 300  
 |||||  
 251 VWSLGITMIEMAILRFPYESWGTFQQLKQVVVEEPPQLPADRFSPFVD 300  
 |||||  
 301 FTAQCLRKNEAERMSYLELI 320  
 |||||  
 301 FTAQCLRKNEAERMSYLEIM 320

Fig. 23(Cont.)





```

1 MPEIRLRHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISSVVLQLE 50
  |||||
1 MPEIRLRHVVCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISSVVLQLE 50
  |||||

51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPSESR 100
  |||||
51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPSESR 100
  |||||

101 SGSNPNRVRMFGDPKLVRAAAEKRWDRVKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
101 SGSNPNRVRMFGDPKLVRAAAEKRWDRVKIVCSQPYSKDSPFGLSFVRFH 150
  |||||

151 SPPDKDEAEAPSQKVTVTKLQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
151 SPPDKDEAEAPSQKVTVTKLQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||

201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESS.....DF 244
  |||||
201 VTASDPAGPSYAAATLQASSAASSASPVSRRAIGSTSKPQESPKGKRKLDL 250
  |||||
245 GGVEEERSWRPQSIPIPSAP 264
  |..:|.|||
251 NOEEKKTPSKPPAQLSPSVP 270

```

Fig. 25

```

1 MPEIRLHVWSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVQLQE 50
  |||
1 MPEIRLHVWSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVQLQE 50
  |||
51 KEEQIHSVDIGNDGSFAFEVLVCGSSAGGAGEQDYEVLLVTSSFMSPSES 100
  |||
51 KEEQIHSVDIGNDGSFAFEVLVCGSSAGGAGEQDYEVLLVTSSFMSPSES 100
  |||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDRVKIVCSQPYSKDSPFGLSEVRFH 150
  |||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDRVKIVCSQPYSKDSPFGLSEVRFH 150
  |||
151 SPPDKDEAEAPSQKVTVTKLQGRVKEEDESANSLRLEDYMSDRVQFV.. 198
  |||
151 SPPDKDEAEAPSQKVTVTKLQGRVKEEDESANSLRPGALFFSRINKTSP 200
  |||
199 ITAQE.WDPSEFEEALMDNPSLA 219
  |||
201 VTASDPAGESYAAATIQASSAA 222

```

**Fig. 26**

[illegible]

Fig. 27

301	GEGTEPRRPRAGPEL	GKILQVVVVLSGQN	PFSELRDKALEL	GAKYR	350
301	GEGTEPRRPRAGPEL	GKILQVVVVLSGQN	PFSELRDKALEL	GAKYR	350
351	PDWTRDSTHLICAFANT	PKYSQVLGLGGRIVR	KEWLDCHRMRRRL	PSRR	400
351	PDWTRDSTHLICAFANT	PKYSQVLGLGGRIVR	KEWLDCHRMRRRL	PSRR	400
401	YLMAGPGSSSEEDASH	SGSGDEAPKLPQKQ	PQTTKTKTQAGP	SSPOK	450
401	YLMAGPGSSSEEDASH	SGSGDEAPKLPQKQ	PQTTKTKTQAGP	SSPOK	450
451	PPTPEETKAASPVLO	EDIDIEGVQSEGQD	NGAEDSGDTEDEL	R RVAEQKE	500
451	PPTPEETKAASPVLO	EDIDIEGVQSEGQD	NGAEDSGDTEDEL	R RVAEQKE	500
501	HLRPFQOENGEDPYAG	STDENTDSEEHQEP	PDLPVPHELPRFL	PGQ	546
501	HLRPFQOENGEDPYAG	STDENTDSEEHQEP	PDLPVPHELPRFL	PGQ	546

**Fig. 27(Cont.)**

```

1  MAGAIASRMSFSSLKRKQPKTFTVRIVTMDAEMEFNCMKWKGDLDLVL 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MAGAIASRMSFSSLKRKQPKTFTVRIVTMDAEMEFNCMKWKGDLDLVL 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 CRTGLRETWFFGLQYTIKDTVAWLKMDKKVLDHDKVSKKEPVTFFHFLAKF 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 CRTGLRETWFFGLQYTIKDTVAWLKMDKKVLDHDKVSKKEPVTFFHFLAKF 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 YPNAEEELVQBITQHLFFQVKKQILDEKIYCPPEASVLLASYAVQAKY 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 YPNAEEELVQBITQHLFFQVKKQILDEKIYCPPEASVLLASYAVQAKY 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 GDYDPSVHKRGFLAQEELLPRVINLYQMTPEMWEERITAWYAEHRGRAR 200
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 GDYDPSVHKRGFLAQEELLPRVINLYQMTPEMWEERITAWYAEHRGRAR 200
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 DEAEMEYLKIAQDLEMYGVNFAIRNKKGTCELLGVDAIGLHIYDPENRL 250
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 DEAEMEYLKIAQDLEMYGVNFAIRNKKGTCELLGVDAIGLHIYDPENRL 250
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 TPKISFPWKNEIRNISYSDEFTIKPLDKKIDVFKFNSSKLRVNKLILQL 300
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 TPKISFPWKNEIRNISYSDEFTIKPLDKKIDVFKFNSSKLRVNKLILQL 299
  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Fig. 28

301 CIGNHDLFMRRRKADSLEVOQKAQAREEKARK..... 333  
 |||||  
 300 CIGNHDLFMRRRKADSLEVOQKAQAREEKARKOMERQRLAREKOMREEA 349  
 334 .....QKKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 371  
 |||||  
 350 ERTRDELEERRLLQKKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 399  
 372 QKAAEAQEMQRIKATAIRTEEEKRIMEQKVLEAEVLALKMAEESERRAK 421  
 |||||  
 400 QKAAEAQEMQRIKATAIRTEEEKRIMEQKVLEAEVLALKMAEESERRAK 449  
 422 EADQLKQDLQEAAREARRAKQKLEIATKPTYPPMNPPIAPLPDIPSFN 471  
 |||||  
 450 EADQLKQDLQEAAREARRAKQKLEIATKPTYPPMNPPIAPLPDIPSFN 499  
 472 LIGDSLSTFDKDTMKRLSMEIEKEKVEYMEKSKHLQEQNLNELKTEIEAL 521  
 |||||  
 500 LIGDSLSTFDKDTMKRLSMEIEKEKVEYMEKSKHLQEQNLNELKTEIEAL 549  
 522 KLKERETALDILHNENSDRGSSKHNTIKKLTILQSAKSRVAFEEEL 567  
 |||||  
 550 KLKERETALDILHNENSDRGSSKHNTIKKLTILQSAKSRVAFEEEL 595

Fig.28 (Cont.)

```

1 MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFGYG 50
  |||||
1 MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFGYG 50
  |||||
51 ASLLCNLIGFGYPAYISIKAIESPKNKDDTQWLTYWVYGVFSIAEFFSD 100
  |||||
51 ASLLCNLIGFGYPAYISIKAIESPKNKDDTQWLTYWVYGVFSIAEFFSD 100
  |||||
101 IFLSWFPFYMLK 113
  |||||
101 IFLSWFPFYMLK 113
  |||||

```

Fig. 29

```

1 MDLEGRNGGAKKNFFKLNKSEKDKEKKPTVSFMSFRYSNWLDKLY 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MDLEGRNGGAKKNFFKLNKSEKDKEKKPTVSFMSFRYSNWLDKLY 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 MVVGTAAIIHGAGLPLMLLVFGEMTDIFANAGNLEDIMSNITNRSDIND 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 MVVGTAAIIHGAGLPLMLLVFGEMTDIFANAGNLEDIMSNITNRSDIND 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 TGFTFNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKRKQ 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 TGFTFNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKRKQ 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
151 FFHAMRQEIGWFDVDHVGENTRLTDDVSKINEVIGDKIGMFFQSMTAF 200
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
151 FFHAMRQEIGWFDVDHVGENTRLTDDVSKINEVIGDKIGMFFQSMTAF 200
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
201 FTGFIVGFTRGWKLTILAIISPVLGLSAAVWAKILSFTDKELLAYAKA 250
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
201 FTGFIVGFTRGWKLTILAIISPVLGLSAAVWAKILSFTDKELLAYAKA 250
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
251 GAVAEVLAAIRTVIAFGQGKELERYNKNLLEEAKRIGIKKAITANISIG 300
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
251 GAVAEVLAAIRTVIAFGQGKELERYNKNLLEEAKRIGIKKAITANISIG 300

```

Fig. 30



301	AAFLLIYASYALAFWYGTTLVLSGEYSICQVLTVFFSVLIGAFSGVQASP	350
301	AAFLLIYASYALAFWYGTTLVLSGEYSICQVLTVFFSVLIGAFSGVQASP	350
351	SIEAFANARGAAVEIFKIIDNKPIDSYSKSGHKPDNIKNLEFRNVHFS	400
351	SIEAFANARGAAVEIFKIIDNKPIDSYSKSGHKPDNIKNLEFRNVHFS	400
401	YPSRKEVKILKGNLKVQSGQTVALVNSGCGKSTTVQLMQRLYDPTGEM	450
401	YPSRKEVKILKGNLKVQSGQTVALVNSGCGKSTTVQLMQRLYDPTGEM	450
451	VSVDGQDIRTINVRFLREIIGVVSQEPVLFTTIAENIRYGRENVTMDEI	500
451	VSVDGQDIRTINVRFLREIIGVVSQEPVLFTTIAENIRYGRENVTMDEI	500
501	EKAVKEANAYDFTMKLPKHFDTLVGERGAQLSGGQKORIAIARALVRNPK	550
501	EKAVKEANAYDFTMKLPKHFDTLVGERGAQLSGGQKORIAIARALVRNPK	550
551	ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVITAG	600
551	ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVITAG	600

**Fig. 30 (Cont.)**

601	FDDGVIVEKGNHDELMKEGIFYFLVTMQTAGNEVELENAADESKSEIDA	650
601	FDDGVIVEKGNHDELMKEGIFYFLVTMQTAGNEVELENAADESKSEIDA	650
651	LEMSSNDSRSSLIKRSTRRSVRGSQAQDRKLSLTKALDESIPPSFWRI	700
651	LEMSSNDSRSSLIKRSTRRSVRGSQAQDRKLSLTKALDESIPPSFWRI	700
701	MKLNLTWPYFVGVFCALINGGLQPAFAIFSKIIIGVTRIDDPETKRQ	750
701	MKLNLTWPYFVGVFCALINGGLQPAFAIFSKIIIGVTRIDDPETKRQ	750
751	NSNLSLLFLALGISFITFTFQGFTEGKAGEILTKRLRYMVFRSMLRQD	800
751	NSNLSLLFLALGISFITFTFQGFTEGKAGEILTKRLRYMVFRSMLRQD	800
801	VSWFDDPKNTTGALTTRLANDAAQVKGAIGSR LAVITQNIANLGTGIIS	850
801	VSWFDDPKNTTGALTTRLANDAAQVKGAIGSR LAVITQNIANLGTGIIS	850
851	FIYGWQITLILLAIVIPIIAAGVYEMKMLSGQALKDKKELEGAGKIATEA	900
851	FIYGWQITLILLAIVIPIIAAGVYEMKMLSGQALKDKKELEGAGKIATEA	900

**Fig. 30 (Cont.)**

901	IENFRTVSLTQEQKFEHMYAQSLQVPRNSLRKAHIFGITFTSFQAMMY	950
901	IENFRTVSLTQEQKFEHMYAQSLQVPRNSLRKAHIFGITFTSFQAMMY	950
951	FSYAGCFRFGAYLVAHKLMSTFEDVLLVFSAVVFGAMAVGVSSFAPDYAK	1000
951	FSYAGCFRFGAYLVAHKLMSTFEDVLLVFSAVVFGAMAVGVSSFAPDYAK	1000
1001	AKISAAHIIMTIEKTPLIDSYSTEGIMPTLEGVNTFGEVFNYPTRPDI	1050
1001	AKISAAHIIMTIEKTPLIDSYSTEGIMPTLEGVNTFGEVFNYPTRPDI	1050
1051	PVLQGLSLEVKKGQTALVGS CGCKSTVVQLLERFYDPLAGKVLLDGKE	1100
1051	PVLQGLSLEVKKGQTALVGS CGCKSTVVQLLERFYDPLAGKVLLDGKE	1100
1101	IKRLNVQWLRHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK	1150
1101	IKRLNVQWLRHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK	1150
1151	EANTHAFIESLPNKYSTKVGDKGTQLSGGQKORIAIARALVRQPHILLD	1200
1151	EANTHAFIESLPNKYSTKVGDKGTQLSGGQKORIAIARALVRQPHILLD	1200

1201 EATSALDTESEKVVQEALDKAREGRTCTIVIAHRLSTIQNADLIIVFQNGR 1250  
 |||||  
 1201 EATSALDTESEKVVQEALDKAREGRTCTIVIAHRLSTIQNADLIIVFQNGR 1250  
 |||||  
 1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT 1277  
 |||||  
 1251 VKEHGTHQQLLAQKGIYFSMVSVQAGT 1277

Fig. 30(Cont.)



```

301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGQASP 350
|||||
301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGQASP 350
|||||
351 SIEAFANARGAAAYEIFKIIDNKPSIDSYKSCHKPDNIKGNLEFRNVHFS 400
|||||
351 SIEAFANARGAAAYEIFKIIDNKPSIDSYKSCHKPDNIKGNLEFRNVHFS 400
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQRLYDPTGEM 450
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQRLYDPTGEM 450
|||||
451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||
451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||
501 ERKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550
|||||
501 ERKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550
|||||
551 ILLDEATSALDTESEAEVQAALDKVSR 578
|||||
551 ILLDEATSALDTESEAVVQVALDKARK 578
|||||

```

Fig. 31(Cont.)

```

1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50

51 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNIIGLLNVFTPKSLEE 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNIIGLLNVFTPKSLEE 100

101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIHR 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIHR 150

151 DLKPSNIVVKSDCTILKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 DLKPSNIVVKSDCTILKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200

201 GYKENTE 207
  | | | | :
201 GYKENVD 207

```

Fig. 32





1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50  
 1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50  
 51 NVAIKKLSRPFQNHAKRAYRELVLKMCVNHKNIIIGLLNVFTPOKSLEE 100  
 51 NVAIKKLSRPFQNHAKRAYRELVLKMCVNHKNIIIGLLNVFTPOKSLEE 100  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIHR 150  
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIHR 150  
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200  
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200  
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPPEFMK 250  
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPPEFMK 250

Fig. 34

```

251 KIQTVRTYVENRPKYAGYSFEKLFDPVLFPADSEHNKLIKASQARDLLSK 300
|||||
251 KIQTVRTYVENRPKYAGYSFEKLFDPVLFPADSEHNKLIKASQARDLLSK 300
|||||
301 MLVIDASKRISVDEALQHPYINWYDPSEAEARSCKL 337
|||||
301 MLVIDASKRISVDEALQHPYINWYDPSEAEAPPKI 337
|||||

```

**Fig. 34(Cont.)**



```

1 MSPFTRIGLSNFDGSCQCGEAVNPYCAVLVKEYVESENGQMYIQKP 50
|
|
|
1 MSPFTRIGLSNFDGSCQCGEAVNPYCAVLVKEYVESENGQMYIQKP 50
|
|
|
51 TMYPPWDSTFDAHINKGRVMQIIVKGKNVDLISSETVELYSLAERCCKNN 100
|
|
|
51 TMYPPWDSTFDAHINKGRVMQIIVKGKNVDLISSETVELYSLAERCCKNN 100
|
|
|
101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFETEGFFALHQRGAIK 150
|
|
|
101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFETEGFFALHQRGAIK 150
|
|
|
151 QAKVHVVKCHEFTATFFPQPTFCVCHFEFVWGLNKQGYQCRQCNAAIHKK 200
|
|
|
151 QAKVHVVKCHEFTATFFPQPTFCVCHFEFVWGLNKQGYQCRQCNAAIHKK 200
|
|
|
201 CIDKVIACKTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
|
|
|
201 CIDKVIACKTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250

```

Fig. 36

```

251 LLWGLARQGLKCDACGMNVHRCQTKVANLGCINOKLMAEALAMTESTQQ 300
|||||
251 LLWGLARQGLKCDACGMNVHRCQTKVANLGCINOKLMAEALAMTESTQQ 300
|||||
301 ARCLRDTEQIFREGPEVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350
|||||
301 ARCLRDTEQIFREGPEVEIGLPCSIKNEARLPCLPTPGKREPQGISWESPL 350
|||||
351 DEVDKMCHLPEPELNKERPSLOIKLKIEDFILHKMLGKSGFGKVFLAEFF 400
|||||
351 DEVDKMCHLPEPELNKERPSLOIKLKIEDFILHKMLGKSGFGKVFLAEFF 400
|||||
401 KTNQFFAIKALKKDVVLMDDDVECTMVKEKRVLSLAWEHPFLTHMFCTFOT 450
|||||
401 KTNQFFAIKALKKDVVLMDDDVECTMVKEKRVLSLAWEHPFLTHMFCTFOT 450
|||||
451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGIQFLHSKGI 500
|||||
451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGIQFLHSKGI 500
|||||

```

Fig. 36 (Cont.)

501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKNTFCGTPDYIAPEI 550  
 |||||  
 501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKNTFCGTPDYIAPEI 550  
 |||||  
 551 LLGQKYNHSDVWSFGVLLIYEMLIGQSPFHGQDEEELFHSIRMDNPFYPR 600  
 |||||  
 551 LLGQKYNHSDVWSFGVLLIYEMLIGQSPFHGQDEEELFHSIRMDNPFYPR 600  
 |||||  
 601 WLEKEAKDLLVK..VRSEAKSVFIR 623  
 |||||  
 601 WLEKEAKDLLVKLFVREPEKRLGVR 625

Fig. 36 (Cont.)